



SEQUENCE LISTING

<110> Johansen, Teit E.
Wen-Yee Saw, Dinah

<110> Novel Neurotrophic Factors

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<140> U.S.S.N 09/804,615

<141> 2001-03-12

<150> DANISH 1998 00904

<151> 1998-07-06

<150> USSN 60/092,229

<151> 1998-07-09

<150> DANISH 1998 01048

<151> 1998-08-19

<150> USSN 60/097,774

<151> 1998-08-25

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<151> 1998-10-06

<150> U.S.S.N 09/347,613

<151> 1999-07-02

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<170> PatentIn Ver. 2.1

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<223> CARBOHYD: Glycosylated Asparagine at Asn87

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<222> (426)..(623)

<223> DISULFID - Cys3-Cys73 disulfide bridge

<222>

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<222> (507)..(707)

<223> DISULFID: Cys35-Cys101 disulfide bridge

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<223> DISULFID: Cys39-Cys103 disulfide bridge

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<222> (616)..(619)

<223> DISULFID: Cys72-Cys72 interchain disulfide bridge

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tcccgaagcc caccctgggtg cccctctttct ccccgaggct ccacttggtc tctccgcgc 119

atg ccc gcc ctg tgg ccc acc ctg gcc gct ctg gct ctg ctg agc agc 167

Met Pro Ala Leu Trp Pro Thr Leu Ala Ala Leu Ala Leu Leu Ser Ser

-75

-90

-85

-80

gtc gca gag gcc tcc ctg gcc tcc gag ccc ccg agc cct gcc ccc ccg 215
 Val Ala Glu Ala Ser Leu Gly Ser Ala Pro Arg Ser Pro Ala Pro Arg
 -75 -70 -65

gaa gcc ccc ccg cct gtc ctg gag tcc ccc gcc gcc ccc ctg ccg ggg 263
 Glu Gly Pro Pro Pro Val Leu Ala Ser Pro Ala Gly His Leu Pro Gly
 -60 -55 -50

gga ccg acc gcc ccg tgg tgc agt gga aga gcc ccg ccg ccg ccg ccg 311
 Gly Arg Thr Ala Arg Trp Cys Ser Gly Arg Ala Arg Arg Pro Arg Arg
 -45 -40 -35

aga ccc ttc tcc gcc ccg gcc ccc gcc gcc tgc acc ccc atc tgc tct 359
 Arg His Phe Ser Ala Arg Ala Pro Ala Ala Cys Thr Pro Ile Cys Ser
 -30 -25 -20

tcc ccg ccg gtc ccg gcc gcc ccg ccg ctg ggg gcc ccg gca gcc ccg tcc 407
 Ser Pro Arg Val Arg Ala Ala Arg Leu Gly Gly Arg Ala Ala Arg Ser
 -15 -10 -5 -1 1

ggc agc ggg gcc gcc gcc tgc ccg ctg ccg tcc cag ctg gtc ccg gtc 455
 Gly Ser Gly Gly Ala Gly Cys Arg Leu Arg Ser Gln Leu Val Pro Val
 5 10 15

ccg gcc ctc gcc ctg gcc ccc ccg tcc gac gag ctg gtc cgt ttc ccg 503
 Arg Ala Leu Gly Leu Gly His Arg Ser Asp Glu Leu Val Arg Phe Arg
 20 25 30

ttc tgc acc gcc tcc tgc ccg ccg gcc ccg tcc cca ccc gac ctc agc 551
 Phe Cys Thr Gly Ser Cys Pro Arg Ala Arg Ser Pro His Asp Leu Ser
 35 40 45

ctg gcc agc cta ctg gcc gcc ggg gcc ctg cga ccg ccc ccg gcc tcc 599
 Leu Ala Ser Leu Leu Gly Ala Gly Ala Leu Arg Pro Pro Pro Gly Ser
 50 55 60 65

ccg ccc gtc agc cag ccc tgc tgc cga ccc acc ccg ccg tac gaa gcc gtc 647
 Arg Pro Val Ser Gln Pro Cys Cys Arg Pro Thr Arg Tyr Glu Ala Val
 70 75 80

tcc ttc atg gac gtc aac agc acc tgg aga acc gtc gac ccg ctc tcc 695
 Ser Phe Met Asp Val Asn Ser Thr Trp Arg Thr Val Asp Arg Leu Ser
 85 90 95

gcc acc gcc tgc gcc tgc ctg gcc tgagggctcg ctccaggggt ttgcagactg 749
 Ala Thr Ala Cys Gly Cys Leu Gly
 100 105

gaccattacc ggtggctctt cctgctggg accctccgc agagtccac tagccaggg 809

cctcagccag ggaagaagg ctcaaagctg agaggccct gccggtgggt gatgga 865

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<212> FRT

<213> Homo sapiens

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Met Pro Ala Leu Trp Pro Thr Leu Ala Ala Leu Ala Leu Leu Ser Ser
-95 -90 -85 -80

Val Ala Glu Ala Ser Leu Gly Ser Ala Pro Arg Ser Pro Ala Pro Arg
-75 -70 -65

Glu Gly Pro Pro Pro Val Leu Ala Ser Pro Ala Gly His Leu Pro Gly
-60 -55 -50

Gly Arg Thr Ala Arg Trp Cys Ser Gly Arg Ala Arg Arg Pro Arg Arg
-45 -40 -35

Arg His Phe Ser Ala Arg Ala Pro Ala Ala Cys Thr Pro Ile Cys Ser
-30 -25 -20

Ser Pro Arg Val Arg Ala Ala Arg Leu Gly Gly Arg Ala Ala Arg Ser
-15 -10 -5 -1 1

Gly Ser Gly Gly Ala Gly Cys Arg Leu Arg Ser Gln Leu Val Pro Val
5 10 15

Arg Ala Leu Gly Leu Gly His Arg Ser Asp Glu Leu Val Arg Phe Arg
20 25 30

Phe Cys Thr Gly Ser Cys Pro Arg Ala Arg Ser Pro His Asp Leu Ser
35 40 45

Leu Ala Ser Leu Leu Gly Ala Gly Ala Leu Arg Pro Pro Pro Gly Ser
50 55 60 65

Arg Pro Val Ser Gln Pro Cys Cys Arg Pro Thr Arg Tyr Glu Ala Val
70 75 80

Ser Phe Met Asp Val Asn Ser Thr Trp Arg Thr Val Asp Arg Leu Ser
85 90 95

Ala Thr Ala Cys Gly Cys Leu Gly

<210> 3
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 <213> Homo sapiens

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 <223> DISULFID: Cys43-Cys108 disulfide bridge

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 <222> (505)..(705)
 <223> DISULFID: Cys70-Cys136 disulfide bridge

<220>
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 <222> (517)..(711)
 <223> DISULFID: Cys74-Cys138 disulfide bridge

<220>
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 <222> (616)..(618)
 <223> DISULFID: Cys107-Cys107 interchain disulfide
 bridge

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 gagccc atg ccc ggc ctg atc tca gcc cga gga cag ccc ctg ctt gag 48
 Met Pro Gly Leu Ile Ser Ala Arg Gly Gln Pro Leu Leu Glu
 -95 -90 -85
 gtc ctt cct ccc caa gcc cac ctg ggt gcc ctg ttt ctg cct gag gct 96
 Val Leu Pro Pro Gln Ala His Leu Gly Ala Leu Phe Leu Pro Glu Ala
 -30 -75 -70
 cca ctt ggt ctg tcc ggc cag cct gcc ctg tgg ccc acc ctg gcc gct 144
 Pro Leu Gly Leu Ser Ala Gln Pro Ala Leu Trp Pro Thr Leu Ala Ala
 -65 -60 -55
 ctg gct ctg ctg agc agc gtc gca gag gcc tcc ctg ggc tcc ggc ccc 192
 Leu Ala Leu Leu Ser Ser Val Ala Glu Ala Ser Leu Gly Ser Ala Pro
 -50 -45 -40
 cgc agc cct gcc ccc cgc gaa ggc ccc cgc cct gtc ctg ggc tcc ccc 240
 Arg Ser Pro Ala Pro Arg Glu Gly Pro Pro Pro Val Leu Ala Ser Pro
 -35 -30 -25 -20
 gcc ggc cac ctg cgc ggc gga cgc acg gcc cgc tgg tgc agt gga aga 288
 Ala Gly His Leu Pro Gly Gly Arg Thr Ala Arg Trp Cys Ser Gly Arg
 -15 -10 -5
 gcc cgc cgc cgc cgc cgc cgc cct tct cgc ccc gag ccc cgc cgc cct 336
 Ala Arg Arg Pro Pro Pro Gln Pro Ser Arg Pro Ala Pro Pro Pro Pro
 -1 1 5 10
 gca ccc cca tct gct ctt ccc cgc ggc ggc cgc ggc ggc cgc gct ggc 384
 Ala Pro Pro Ser Ala Leu Pro Arg Gly Gly Arg Ala Ala Arg Ala Gly
 15 20 25

ggc cgg ggc aac cgc gct cgg qca ggc ggg ggc cgg ggc tgc cgc ctg 432
 Gly Pro Gly Asn Arg Ala Arg Ala Ala Gly Ala Arg Gly Cys Arg Leu
 30 35 40 45

cgc tgc cag ctg gtg cgg gtg cgc ggc ctg ggc ctg ggc cgc cgc tgc 480
 Arg Ser Gln Leu Val Pro Val Arg Ala Leu Gly Leu Gly His Arg Ser
 50 55 60

gac gag ctg gtg cgt ttc cgc ttc tgc agc ggc tgc tgc cgc cgc ggc 528
 Asp Glu Leu Val Arg Phe Arg Phe Cys Ser Gly Ser Cys Arg Arg Ala
 65 70 75

cgc tct cca cgc gac ctg agc ctg ggc agc cta ctg ggc ggc ggc ggc 576
 Arg Ser Pro His Asp Leu Ser Leu Ala Ser Leu Leu Gly Ala Gly Ala
 80 85 90

ctg cga cgg ccc cgg ggc tgc cgg ccc gtc agc cag ccc tgc tgc cga 624
 Leu Arg Pro Pro Pro Gly Ser Arg Pro Val Ser Gln Pro Cys Cys Arg
 95 100 105

ccc acg cgc tac gaa ggc gtc tgc ttc atg gac gtc aac agc acc tgg 672
 Pro Thr Arg Tyr Glu Ala Val Ser Phe Met Asp Val Asn Ser Thr Trp
 110 115 120 125

aga acc gtg gac cgc ctg tgc ggc aac ccc tgc ggc tgc ctg ggc 717
 Arg Thr Val Asp Arg Leu Ser Ala Asn Pro Cys Gly Cys Leu Gly
 130 135 140

tgagggtctg ctccagggt ttgcagaatg gacccattacc ggtggtcttt cctgcttggg 777

accctccgc agagtccac tagccagcgg cctcagccag ggacgaagga ctcaaagctg 837

agaggccct gccgggtgggt gatg 861

<210> 4

<211> 237

<212> PRT

<213> Homo sapiens

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Met Pro Gly Leu Ile Ser Ala Arg Gly Gln Pro Leu Leu Glu Val Leu
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Pro Pro Gln Ala His Leu Gly Ala Leu Phe Leu Pro Glu Ala Pro Leu
 -30 -25 -20

Gly Leu Ser Ala Gln Pro Ala Leu Trp Pro Thr Leu Ala Ala Leu Ala

-65		-60		-55		-50									
Leu	Leu	Ser	Ser	Val	Ala	Glu	Ala	Ser	Leu	Gly	Ser	Ala	Pro	Arg	Ser
				-45					-40					-35	
Pro	Ala	Pro	Arg	Glu	Gly	Pro	Pro	Pro	Val	Leu	Ala	Ser	Pro	Ala	Gly
			-30					-25					-20		
His	Leu	Pro	Gly	Gly	Arg	Thr	Ala	Arg	Trp	Cys	Ser	Gly	Arg	Ala	Arg
		-15					-10					-5			
Arg	Pro	Pro	Pro	Gln	Pro	Ser	Arg	Pro	Ala	Pro	Pro	Pro	Pro	Ala	Pro
-1	1				5					10					15
Pro	Ser	Ala	Leu	Pro	Arg	Gly	Gly	Arg	Ala	Ala	Arg	Ala	Gly	Gly	Pro
			20					25					30		
Gly	Asn	Arg	Ala	Arg	Ala	Ala	Gly	Ala	Arg	Gly	Cys	Arg	Leu	Arg	Ser
			35					40					45		
Gln	Leu	Val	Pro	Val	Arg	Ala	Leu	Gly	Leu	Gly	His	Arg	Ser	Asp	Glu
		50					55					60			
Leu	Val	Arg	Phe	Arg	Phe	Cys	Ser	Gly	Ser	Cys	Arg	Arg	Ala	Arg	Ser
	65					70				75					
Pro	His	Asp	Leu	Ser	Leu	Ala	Ser	Leu	Leu	Gly	Ala	Gly	Ala	Leu	Arg
80					85					90					95
Pro	Pro	Pro	Gly	Ser	Arg	Pro	Val	Ser	Gln	Pro	Cys	Cys	Arg	Pro	Thr
			100						105					110	
Arg	Tyr	Glu	Ala	Val	Ser	Phe	Met	Asp	Val	Asn	Ser	Thr	Trp	Arg	Thr
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Val	Asp	Arg	Leu	Ser	Ala	Asn	Pro	Cys	Gly	Cys	Leu	Gly			
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<223> Wherein Xaa at position 134 designates Asn or Thr,
and Xaa at position 135 designates Ala or Pro

4400> 5

Pro Pro Pro Gln Pro Ser Arg Pro Ala Pro Pro Pro Ala Pro Pro
1 5 10 15

Ser Ala Leu Pro Arg Gly Gly Arg Ala Ala Arg Ala Gly Gly Pro Gly
20 25 30

Asn Arg Ala Arg Ala Ala Gly Ala Arg Gly Cys Arg Leu Arg Ser Gln
35 40 45

Leu Val Pro Val Arg Ala Leu Gly Leu Gly His Arg Ser Asp Glu Leu
50 55 60

Val Arg Phe Arg Phe Cys Ser Gly Ser Cys Arg Arg Ala Arg Ser Pro
65 70 75 80

His Asp Leu Ser Leu Ala Ser Leu Leu Gly Ala Gly Ala Leu Arg Pro
85 90 95

Pro Pro Gly Ser Arg Pro Val Ser Gln Pro Cys Cys Arg Pro Thr Arg
100 105 110

Tyr Glu Ala Val Ser Phe Met Asp Val Asn Ser Thr Trp Arg Thr Val
115 120 125

Asp Arg Leu Ser Ala Xaa Xaa Cys Gly Cys Leu Gly
130 135 140

42100> 6

42110> 116

42120> PRT

42130> Homo sapiens

42200>

42230> Wherein Xaa at position 110 designates Asn or Thr,
and Xaa at position 111 designates Ala or Pro

4400> 6

Ala Ala Arg Ala Gly Gly Pro Gly Asn Arg Ala Arg Ala Ala Gly Ala
1 5 10 15

Arg Gly Cys Arg Leu Arg Ser Gln Leu Val Pro Val Arg Ala Leu Gly
20 25 30

Leu Gly His Arg Ser Asp Glu Leu Val Arg Phe Arg Phe Cys Ser Gly
35 40 45

Ser Cys Arg Arg Ala Arg Ser Pro His Asp Leu Ser Leu Ala Ser Leu
50 55 60

Leu Gly Ala Gly Ala Leu Arg Pro Pro Pro Gly Ser Arg Pro Val Ser
65 70 75 80

Gln Pro Cys Cys Arg Pro Thr Arg Tyr Glu Ala Val Ser Phe Met Asp
85 90 95

Val Asn Ser Thr Trp Arg Thr Val Asp Arg Leu Ser Ala Xaa Xaa Cys
100 105 110

Gly Cys Leu Gly
115

<210> 7

<211> 113

<212> PRT

<213> Homo sapiens

<220>

<223> Wherein Xaa at position 107 designates Asn or Thr,
and Xaa at position 108 designates Ala or Pro

<400> 7

Ala Gly Gly Pro Gly Asn Arg Ala Arg Ala Ala Gly Ala Arg Gly Cys
1 5 10 15

Arg Leu Arg Ser Gln Leu Val Pro Val Arg Ala Leu Gly Leu Gly His
20 25 30

Arg Ser Asp Glu Leu Val Arg Phe Arg Phe Cys Ser Gly Ser Cys Arg
35 40 45

Arg Ala Arg Ser Pro His Asp Leu Ser Leu Ala Ser Leu Leu Gly Ala
50 55 60

Gly Ala Leu Arg Pro Pro Pro Gly Ser Arg Pro Val Ser Gln Pro Cys
65 70 75 80

Cys Arg Pro Thr Arg Tyr Glu Ala Val Ser Phe Met Asp Val Asn Ser
85 90 95

Thr Trp Arg Thr Val Asp Arg Leu Ser Ala Xaa Xaa Cys Gly Cys Leu
100 105 110

Gly

<210> 8
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<212> DNA
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<223> CARBOHYD: glycosylated asparagine at Asn122

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<223> DISULFID: Gly43-Gly108 disulfide bridge

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<211> misc_structure
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 <213> DISULFID: Gly70-Gly136 disulfide bridge

<210>
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 <212> (517)..(711)
 <213> DISULFID: Gly74-Gly138 disulfide bridge

<210>
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 <212> (616)..(613)
 <213> DISULFID: Gly107-Gly107 interchain disulfide
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 atg gaa ctt gga ctt gga ggc ctc tcc aag ctg tcc cac tgc ccc tgg 105
 Met Glu Leu Gly Leu Gly Gly Leu Ser Thr Leu Ser His Cys Pro Trp
 -30 -75 -70 -65
 cct agg cgg cag cct gcc ctg tgg ccc acc ctg gcc gct ctg gct ctg 153
 Pro Arg Arg Gln Pro Ala Leu Trp Pro Thr Leu Ala Ala Leu Ala Leu
 -60 -55 -50
 ctg agc agc gtc gca gag gcc tcc ctg ggc tcc gag ccc cgc agc cct 201
 Leu Ser Ser Val Ala Glu Ala Ser Leu Gly Ser Ala Pro Arg Ser Pro
 -45 -40 -35
 gcc ccc cgc gaa ggc ccc ccg cct gtc ctg gag tcc ccc gcc ggc cac 249
 Ala Pro Arg Glu Gly Pro Pro Pro Val Leu Ala Ser Pro Ala Gly His
 -30 -25 -20
 ctg ccg ggg gga cgc aag gcc cgc tgg tgc agt gga aga gcc cgg cgg 297
 Leu Pro Gly Gly Arg Thr Ala Arg Trp Cys Ser Gly Arg Ala Arg Arg
 -15 -10 -5 -1
 ccg ccg ccg cag cct tct cgg ccc gag ccc ccg ccg cct gca ccc cca 345
 Pro Pro Pro Gln Pro Ser Arg Pro Ala Pro Pro Pro Pro Ala Pro Pro
 1 5 10 15
 tct gct ctt ccc cgc ggg ggc cgc gag ggc cgg gct ggg ggc ccg ggc 393
 Ser Ala Leu Pro Arg Gly Gly Arg Ala Ala Arg Ala Gly Gly Pro Gly
 20 25 30
 agc cgc gct cgg gca ggc ggg gag cgg ggc tgc cgc ctg cgc tgc cag 441
 Ser Arg Ala Arg Ala Ala Gly Ala Arg Gly Cys Arg Leu Arg Ser Gln

35

40

45

ctg gtg cgg gtg cgc ggc ctc ggc ctg ggc cac cgc tcc gac gag ctg 489
 Leu Val Pro Val Arg Ala Leu Gly Leu Gly His Arg Ser Asp Glu Leu
 50 55 60

gtg cgt ttc cgc ttc tgc agc ggc tcc tgc cgc cgc gag cgc tct cca 537
 Val Arg Phe Arg Phe Cys Ser Gly Ser Cys Arg Arg Ala Arg Ser Pro
 65 70 75 80

cac gac ctc agc ctg gcc agc cta ctg ggc gcc ggg gcc ctg cga cgg 585
 His Asp Leu Ser Leu Ala Ser Leu Leu Gly Ala Gly Ala Leu Arg Pro
 85 90 95

ccc cgg ggc tcc cgg ccc gtc agc cag ccc tgc tgc cga ccc acg cgc 633
 Pro Pro Gly Ser Arg Pro Val Ser Gln Pro Cys Cys Arg Pro Thr Arg
 100 105 110

tac gaa gag gtc tcc ttc atg gac gtc aac agc acc tgg aga acc gtg 681
 Tyr Glu Ala Val Ser Phe Met Asp Val Asn Ser Thr Trp Arg Thr Val
 115 120 125

gac cgc ctc tcc gcc acc gcc tgc ggc tgc ctg ggc tgagggtctg 727
 Asp Arg Leu Ser Ala Thr Ala Cys Gly Cys Leu Gly
 130 135 140

ctccagggct ttgcagactg gacccttacc ggtggctctt cctgcctggg accctccgc 787

agagtccac tagccagcgg cctcagccag ggaagaagga ctcaaagctg agaggccct 847

acgggtgggt gatg 861

<210> 9

<211> 220

<212> FRT

<213> Homo sapiens

<400> 9

Met Glu Leu Gly Leu Gly Gly Leu Ser Thr Leu Ser His Cys Pro Trp
 -80 -75 -70 -65

Pro Arg Arg Gln Pro Ala Leu Trp Pro Thr Leu Ala Ala Leu Ala Leu
 -60 -55 -50

Leu Ser Ser Val Ala Glu Ala Ser Leu Gly Ser Ala Pro Arg Ser Pro
 -45 -40 -35

Ala Pro Arg Glu Gly Pro Pro Pro Val Leu Ala Ser Pro Ala Gly His
 -30 -25 -20

Leu Pro Gly Gly Arg Thr Ala Arg Trp Cys Ser Gly Arg Ala Arg Arg
 -15 -10 -5 -1

Pro Pro Pro Gln Pro Ser Arg Pro Ala Pro Pro Pro Pro Ala Pro Pro
 1 5 10 15

Ser Ala Leu Pro Arg Gly Gly Arg Ala Ala Arg Ala Gly Gly Pro Gly
 20 25 30

Ser Arg Ala Arg Ala Ala Gly Ala Arg Gly Cys Arg Leu Arg Ser Gln
 35 40 45

Leu Val Pro Val Arg Ala Leu Gly Leu Gly His Arg Ser Asp Glu Leu
 50 55 60

Val Arg Phe Arg Phe Cys Ser Gly Ser Cys Arg Arg Ala Arg Ser Pro
 65 70 75 80

His Asp Leu Ser Leu Ala Ser Leu Leu Gly Ala Gly Ala Leu Arg Pro
 85 90 95

Pro Pro Gly Ser Arg Pro Val Ser Gln Pro Cys Cys Arg Pro Thr Arg
 100 105 110

Tyr Glu Ala Val Ser Phe Met Asp Val Asn Ser Thr Trp Arg Thr Val
 115 120 125

Asp Arg Leu Ser Ala Thr Ala Cys Gly Cys Leu Gly
 130 135 140

02100 10

02110 140

02120 PRT

02130 Homo sapiens

02200

02210 CARBOHYD

02220 (122)

02230 glycosylated asparagine

04000 10

Pro Pro Pro Gln Pro Ser Arg Pro Ala Pro Pro Pro Pro Ala Pro Pro
 1 5 10 15

Ser Ala Leu Pro Arg Gly Gly Arg Ala Ala Arg Ala Gly Gly Pro Gly
 20 25 30

Ser Arg Ala Arg Ala Ala Gly Ala Arg Gly Cys Arg Leu Arg Ser Gln
 35 40 45

Leu Val Pro Val Arg Ala Leu Gly Leu Gly His Arg Ser Asp Glu Leu
 50 55 60

Val Arg Phe Arg Phe Cys Ser Gly Ser Cys Arg Arg Ala Arg Ser Pro
 65 70 75 80

His Asp Leu Ser Leu Ala Ser Leu Leu Gly Ala Gly Ala Leu Arg Pro
 85 90 95

Pro Pro Gly Ser Arg Pro Val Ser Gln Pro Cys Cys Arg Pro Thr Arg
 100 105 110

Tyr Glu Ala Val Ser Phe Met Asp Val Asn Ser Thr Trp Arg Thr Val
 115 120 125

Asp Arg Leu Ser Ala Thr Ala Cys Gly Cys Leu Gly
 130 135 140

<110> 11

<111> 116

<112> PRT

<113> Homo sapiens

<120>

<121> CARBOHYD

<122> (93)

<123> glycosylated asparagine

<400> 11

Ala Ala Arg Ala Gly Gly Pro Gly Ser Arg Ala Arg Ala Ala Gly Ala
 1 5 10 15

Arg Gly Cys Arg Leu Arg Ser Gln Leu Val Pro Val Arg Ala Leu Gly
 20 25 30

Leu Gly His Arg Ser Asp Glu Leu Val Arg Phe Arg Phe Cys Ser Gly
 35 40 45

Ser Cys Arg Arg Ala Arg Ser Pro His Asp Leu Ser Leu Ala Ser Leu
 50 55 60

Leu Gly Ala Gly Ala Leu Arg Pro Pro Pro Gly Ser Arg Pro Val Ser
65 70 75 80

Gln Pro Cys Cys Arg Pro Thr Arg Tyr Glu Ala Val Ser Phe Met Asp
85 90 95

Val Asn Ser Thr Trp Arg Thr Val Asp Arg Leu Ser Ala Thr Ala Cys
100 105 110

Gly Cys Leu Gly
115

<210> 12

<211> 113

<212> PRT

<213> Homo sapiens

<220>

<221> CARBOHYD

<222> (95)

<223> glycosylated asparagine

<400> 12

Ala Gly Gly Pro Gly Ser Arg Ala Arg Ala Ala Gly Ala Arg Gly Cys
1 5 10 15

Arg Leu Arg Ser Gln Leu Val Pro Val Arg Ala Leu Gly Leu Gly His
20 25 30

Arg Ser Asp Glu Leu Val Arg Phe Arg Phe Cys Ser Gly Ser Cys Arg
35 40 45

Arg Ala Arg Ser Pro His Asp Leu Ser Leu Ala Ser Leu Leu Gly Ala
50 55 60

Gly Ala Leu Arg Pro Pro Pro Gly Ser Arg Pro Val Ser Gln Pro Cys
65 70 75 80

Cys Arg Pro Thr Arg Tyr Glu Ala Val Ser Phe Met Asp Val Asn Ser
85 90 95

Thr Trp Arg Thr Val Asp Arg Leu Ser Ala Thr Ala Cys Gly Cys Leu
100 105 110

Gly

<210> 13
 <211> 102
 <212> DNA
 <213> Homo sapiens

<400> 13
 ccaggccagc ctactggggg ccggggccct ggcacggccc ccgggtccc ggcccgtcag 60
 ccagccctgc tgcggaccca ccggtacga agcgggtccc tt 102

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 <212> DNA
 <213> Murinae gen. sp.

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 ccgcccagc agcatctcag tctggccagc ctactggggg ctggggccct acggtcgct 120
 ccgggtccc ggccgatcag ccagccctgc tgcgggccc ctgcctatga ggccgtctcc 180
 ttcctggagc tgaacagcac ctggagaaac gtggacggcc 220

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 <213> Murinae gen. sp.

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 ccggtccga gggcggagc gccaggtgag cctgaaagg tggggcggg ccggggcgct 180
 ctgggcccc ccccgggatc tggtagccc ggggtctgaa ttgacaccc gacgggggag 240
 ggcaggagc cgtcaggga tggattggg ctgggcccc agatgggccc ccggggctct 300
 gccagcaaca agtccctgg gccccagccc cctctggac tggggcttgg agccctgac 360
 ccaaggcac agacgggtg ccaaggcccc acctttaact aaaagaggc ctggcaggtg 420

cacaactctg ggcattgatcc acttgagctt cgggggaaag ccagcactg gtcccaggag 481
 agggccttag aaggatacgg accaggaccc ctttggtatg gaggtaacgc tgagcatgga 541
 gtggaaggaa cccagttac taattctctc aaccacctg gtaccttcag cctgaagta 601
 cagagcagaa ggtctctaga agacaggacc acagctgtgt gaggctcccc cctgaggcct 660
 tagacgatct ctgagctcag ctgagctttg ttgcccata tggagaagtg agccattgat 720
 tgacctctgt gccttcggaa ggaacaggtc ctgccaagca cctaaccacg agagcaaggt 780
 tctccatcgc agctaccgtc gctgagttga ctctagctac tccacctctc tgggtcgttt 840
 cgagagactg gaggggaagg aggaataccc caaaggataa ctaactcact tttcagtttg 900
 caagctgccc cagggaaggg gtggggaaac ggggtccacg aggtctctga tgggagcttc 960

tggagccgaa agct atg gaa ctg gga ctt gca gag cct act gca ttg tcc 1010
 Met Glu Leu Gly Leu Ala Glu Pro Thr Ala Leu Ser
 1 5 10

cac tgc ctc cgg cct agg tgg cag tca gcc tgg tgg cca acc cta gct 1058
 His Cys Leu Arg Pro Arg Trp Gln Ser Ala Trp Trp Pro Thr Leu Ala
 15 20 25

gtt cta gcc ctg ctg agc tgc gtc aca gaa gct tcc ctg gac cca atg 1106
 Val Leu Ala Leu Leu Ser Cys Val Thr Glu Ala Ser Leu Asp Pro Met
 30 35 40

tcc cgc agc ccc gcc gct cgc gac ggt ccc tca ccg gtc ttg gcg ccc 1154
 Ser Arg Ser Pro Ala Ala Arg Asp Gly Pro Ser Pro Val Leu Ala Pro
 45 50 55 60

ccc acg gac cac ctg cct ggg gga cac act gcg cat ttg tgc agc gaa 1202
 Pro Thr Asp His Leu Pro Gly Gly His Thr Ala His Leu Cys Ser Glu
 65 70 75

aga acc ctg cga ccc ccg cct cag tct cct cag ccc gca ccc ccg ccg 1250
 Arg Thr Leu Arg Pro Pro Pro Gln Ser Pro Gln Pro Ala Pro Pro Pro
 80 85 90

cct ggt ccc gcg ctc cag tct cct ccc gct gcg ctc cgc ggg gca cgc 1298
 Pro Gly Pro Ala Leu Gln Ser Pro Pro Ala Ala Leu Arg Gly Ala Arg
 95 100 105

gcg gcg cgt gca gga acc ccg agc agc cgc gca ccg acc aca gat gcg 1346
 Ala Ala Arg Ala Gly Thr Arg Ser Ser Arg Ala Arg Thr Thr Asp Ala

110

115

120

ogc ggc tgc cgc ctg cgc tog cag ctg gtg ccg gtg agc ggc ctc ggc 1394
 Arg Gly Cys Arg Leu Arg Ser Gln Leu Val Pro Val Ser Ala Leu Gly
 125 130 135 140

cta ggc cag agc tcc gac gag ctg ata cgt ttc cgc ttc tgc agc ggc 1442
 Leu Gly His Ser Ser Asp Glu Leu Ile Arg Phe Arg Phe Cys Ser Gly
 145 150 155

tog tgc cgc cga gca cgc tcc cag cag gat ctc agt ctg gcc agc cta 1490
 Ser Cys Arg Arg Ala Arg Ser Gln His Asp Leu Ser Leu Ala Ser Leu
 160 165 170

ctg ggc gct ggc gcc cta cgc tog cct ccc ggc tcc cgc ccg atc agc 1538
 Leu Gly Ala Gly Ala Leu Arg Ser Pro Pro Gly Ser Arg Pro Ile Ser
 175 180 185

cag ccc tgc tgc cgc ccc act cgc tat gag gcc gtc tcc ttc atg gac 1586
 Gln Pro Cys Cys Arg Pro Thr Arg Tyr Glu Ala Val Ser Phe Met Asp
 190 195 200

gtg aac agc acc tgg agg acc gtg gac cag ctc tcc gcc act gcc tgc 1634
 Val Asn Ser Thr Trp Arg Thr Val Asp His Leu Ser Ala Thr Ala Cys
 205 210 215 220

ggc tgt ctg ggc tgaggatgat ctatctccaa gcttttgac actagaccaa 1686
 Gly Cys Leu Gly

tctgttgccc taactgggaa agctccaccc ggcctcacta accaggagcc tcaactcagc 1746

aggatatgga ggcctgcagag ctcaggccccc aggcgggtga gtgacagacg tcgtcgccat 1806

gacagacaga gtgaaagatg tcggaacccc tgaccaacag tcccaagttg ttcattggatc 1866

ccagctctac agacaggaga aacctcagct aaagagaact cctctgggag aatccagaaa 1926

tggccctctg tccctggggaa tgaattttga agagatatat atacatatat acattgtagt 1986

ccggttgcctg gaccagcctg tcttgaaaac agtcgggtgt tcacttctgg aagccgaagc 2046

cctatttatt attctcacaat tatttattta ctttgaaaaa aaacggccaa gtgggctctc 2106

ctttagtgag ggttaatttg tgatcccggt 2136

210> 16

211> 224

<212> PRT

<213> Murinae gen. sp.

<400> 16

Met Glu Leu Gly Leu Ala Glu Pro Thr Ala Leu Ser His Cys Leu Arg
1 5 10 15

Pro Arg Trp Gln Ser Ala Trp Trp Pro Thr Leu Ala Val Leu Ala Leu
20 25 30

Leu Ser Cys Val Thr Glu Ala Ser Leu Asp Pro Met Ser Arg Ser Pro
35 40 45

Ala Ala Arg Asp Gly Pro Ser Pro Val Leu Ala Pro Pro Thr Asp His
50 55 60

Leu Pro Gly Gly His Thr Ala His Leu Cys Ser Glu Arg Thr Leu Arg
65 70 75 80

Pro Pro Pro Gln Ser Pro Gln Pro Ala Pro Pro Pro Pro Gly Pro Ala
85 90 95

Leu Gln Ser Pro Pro Ala Ala Leu Arg Gly Ala Arg Ala Ala Arg Ala
100 105 110

Gly Thr Arg Ser Ser Arg Ala Arg Thr Thr Asp Ala Arg Gly Cys Arg
115 120 125

Leu Arg Ser Gln Leu Val Pro Val Ser Ala Leu Gly Leu Gly His Ser
130 135 140

Ser Asp Glu Leu Ile Arg Phe Arg Phe Cys Ser Gly Ser Cys Arg Arg
145 150 155 160

Ala Arg Ser Gln His Asp Leu Ser Leu Ala Ser Leu Leu Gly Ala Gly
165 170 175

Ala Leu Arg Ser Pro Pro Gly Ser Arg Pro Ile Ser Gln Pro Cys Cys
180 185 190

Arg Pro Thr Arg Tyr Glu Ala Val Ser Phe Met Asp Val Asn Ser Thr
195 200 205

Trp Arg Thr Val Asp His Leu Ser Ala Thr Ala Cys Gly Cys Leu Gly
210 215 220

<210> 17

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR Primer

<400> 17

ccgggccagc ctactggg

18

<210> 18

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR Primer

<400> 18

aaaggagacgg ctctgtatgg

20

<210> 19

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR Primer

<400> 19

atgggaacttg gacttgg

17

<210> 20

<211> 16

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR Primer

<400> 20

tccatcaccc accggc

16

<210> 21
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR Primer

<400> 21
ggcacccgct cagacgag 18

<210> 22
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR Primer

<400> 22
ggcgggtccac ggttctccag 20

<210> 23
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR Primer

<400> 23
ccaagccac ctgggtgccc tttttctcc 29

<210> 24
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR Primer

<400> 24
catcacccac cggcaggggc ctctccag 27

<210> 25
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR Primer

<400> 35
gagggcctgc cgggctgat ctcagcccca ggaca 35

<210> 26
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR Primer

<400> 26
ccctggctga ggccgctggc tagtgggaact ctgc 34

<210> 27
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Hybridization
Probe

<400> 27
ncaggtagtc cgtggggggc gccaaagaccg g 31

<210> 18
<211> 16
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR primer

<400> 28
ctaggagccc atgccc 16

<210> 29
 <211> 351
 <212> DNA
 <213> Homo sapiens

<400> 29
 atggctggag gaccgggac tcgtgtcgt gcagcaggag cactgggtg tcgtctggt 60
 tctcaactag tggcgggtgg tgcactcgga ctgggacacc gtcccgacga actagtaagt 120
 ttctgttttt gttcaggatc ttgtgtcgt gcacgttctc cgcctgatct atctctagca 180
 tctctactag gaccgggag actaagaacg ccgcccggat ctgacctgt atctcaact 240
 tgttgtagac ctactagata cgaagcagta tcttctatgg acgtaaaact tacatggaga 300
 accgttagata gactatctgc aacgcgatgt ggtgtctag gatgataata g 351

<210> 30
 <211> 414
 <212> DNA
 <213> Homo sapiens

<400> 30
 atggggccatc atcctcatca tcatcatcat cactactcga ggggccatat cgaacgacga 60
 gacaagggtg gaggacggg atctcgtgt cgtgcagcag gaggacgtgg ctgtcgtctg 120
 cgttctcacc tagtgcgggt ggtgcactc ggactgggac accgttcga cgaactagta 180
 cgttctcgtt ttgttcagg atcttctgt cgtgcacgtt ctccgatga tctatctcta 240
 gcatctctac taggagccgg agcactaaga ccgcccggg gatctagacc tgtatctcaa 300
 ccttgtttga gacctactag atacgaagca gtatcttcca tggacgtaaa ctctacatgg 360
 agaaccgtag atagactatc tgcaaccgca tgtggtgtc taggatgata atag 414

<210> 31
 <211> 39
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: PCR primer

<400> 31
 gaggaaaaaa ggcgcgcga tggaaattgg atttggagg 39

<210> 32
 <211> 39
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR primer

<400> 32

ttttttcttt ggaggccgct cagcccaggg agccgcagg

39

<210> 33

<211> 16

<212> DNA

<213> Artificial Sequence

<210>

<213> Description of Artificial Sequence: primer

<400> 33

gagagagccc tcagcc

16

<210> 34

<211> 224

<212> PRT

<213> Rattus sp.

<400> 34

Met Glu Leu Gly Leu Gly Glu Pro Thr Ala Leu Ser His Cys Leu Arg

1

5

10

15

Pro Arg Trp Gln Pro Ala Leu Trp Pro Thr Leu Ala Ala Leu Ala Leu

20

25

30

Leu Ser Ser Val Thr Glu Ala Ser Leu Asp Pro Met Ser Arg Ser Pro

35

40

45

Ala Ser Arg Asp Val Pro Ser Pro Val Leu Ala Pro Pro Thr Asp Tyr

50

55

60

Leu Pro Gly Gly His Thr Ala His Leu Cys Ser Glu Arg Ala Leu Arg

65

70

75

80

Pro Pro Pro Gln Ser Pro Gln Pro Ala Pro Pro Pro Pro Gly Pro Ala

85

90

95

Leu Gln Ser Pro Pro Ala Ala Leu Arg Gly Ala Arg Ala Ala Arg Ala

100

105

110

Gly Thr Arg Ser Ser Arg Ala Arg Ala Thr Asp Ala Arg Gly Cys Arg

115

120

125

Leu Arg Ser Gln Leu Val Pro Val Ser Ala Leu Gly Leu Gly His Ser
 130 135 140

Ser Asp Glu Leu Ile Arg Phe Arg Phe Cys Ser Gly Ser Cys Arg Arg
 145 150 155 160

Ala Arg Ser Pro His Asp Leu Ser Leu Ala Ser Leu Leu Gly Ala Gly
 165 170 175

Ala Leu Arg Ser Pro Pro Gly Ser Arg Pro Ile Ser Gln Pro Cys Cys
 180 185 190

Arg Pro Thr Arg Tyr Glu Ala Val Ser Phe Met Asp Val Asn Ser Thr
 195 200 205

Trp Arg Thr Val Asp His Leu Ser Ala Thr Ala Cys Gly Cys Leu Gly
 210 215 220

<210> 35

<211> 365

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:synthetic gene
 for Neublabin

<400> 35

taccatggct ggaggacgg gatctgtgc tegtgcagca ggagcacgtg gctgtgtct 60
 gggtctcaa ctagtgcgg tgggtgcaat cggactggga caccgttcg accaactagt 120
 acgttttctg tttgttcag gatctgtgog tegtgcacgt tctcgcacg atctatctct 180
 agpatctcta ctaggagcgg gagcaactaag accgcgcgg ggatctagac ctgtatctca 240
 acctgttgt agactacta gatacgaagc agtatcttct atggacgtaa actctacatg 300
 gagaacgta gatagactat ctgcaacgc atgtggctgt ctaggatgat aatagggatc 360
 cgtct 365

<210> 36

<211> 365

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:synthetic gene

for Neublabin

<400> 36

```
atgggtacga cctcctggcc ctagagcaag agcaagtcgt cctcgtgcac cgacagcaga 60
cgcaagagtt gatcaaggcc acgcacgtga gctgaccct gtggcaagga tgcttgatca 120
tgcaaaaagca aaaacaagtc ctagaacaga agcaagtgca agaggcgtac tagatagaga 180
tcgtagagat gatcctcgga ctctgtgatt tggcggcgga cctagatctg gacatagagt 240
tggaacaaca totggatgat ctatgcttgg tcatagaaaag tacctgcatt tgagatgtac 300
ctcttggaat ctatctgata gacgttggcg tacacgcaga gatcctaata ttatcctag 360
gcaga
```

<410> 37

<411> 114

<412> PRT

<413> Artificial Sequence

<420>

<423> Description of Artificial Sequence:synthetic
Neublabin

<400> 37

```
Met Ala Gly Gly Pro Gly Ser Arg Ala Arg Ala Ala Gly Ala Arg Gly
  1           5           10          15
```

```
Cys Arg Leu Arg Ser Gln Leu Val Pro Val Arg Ala Leu Gly Leu Gly
      20           25           30
```

```
His Arg Ser Asp Glu Leu Val Arg Phe Arg Phe Cys Ser Gly Ser Cys
      35           40           45
```

```
Arg Arg Ala Arg Ser Pro His Asp Leu Ser Leu Ala Ser Leu Leu Gly
      50           55           60
```

```
Ala Gly Ala Leu Arg Pro Pro Pro Gly Ser Arg Pro Val Ser Gln Pro
      65           70           75           80
```

```
Cys Cys Arg Pro Thr Arg Tyr Glu Ala Val Ser Phe Met Asp Val Asn
      85           90           95
```

```
Ser Thr Trp Arg Thr Val Asp Arg Leu Ser Ala Thr Ala Cys Gly Cys
     100          105          110
```

Leu Gly

<410> 38

*211 - 442

*212 - DNA

*213 - Artificial Sequence

*220 -

*223 - Description of Artificial Sequence:synthetic gene
gene for HisNeublastin

*400 - 38

```
tacatgggc catcatcatc atcatcatca tcatcatcac tcgagcgggc atatcgacga 60
cgagacaaag gctggaggac cgggatctcg tgcctgtgca gcaggagcac gtggctgtcg 120
tcctggttct caactagtgc cggtgcggtg actcggaact ggacacggtt ccgacgaact 180
agtaagtttt cgtttttggt caggatcttg tcctgtgca cgtttctcgc atgatctatc 240
ctctgcatct ctactaggag ccggagcaact aagacgcgcg ccgggatcta gacctgtatc 300
tcacacctgt tctagaacta ctagatacga agcagtatct ttcattggac taaactctac 360
atggagaacc gtagatagac tatctgcaac cgcattgtgc tgtctaggat gataataggg 420
atccggctgc taacaaagcc cg                                     442
```

*210 - 39

*211 - 442

*212 - DNA

*213 - Artificial Sequence

*220 -

*223 - Description of Artificial Sequence:synthetic gene
for HisNeublastin

*400 - 39

```
atggtagccg gtagtagtag tagtagtagt agtagtagtg agctcgccgg tatagctgct 60
gctgctgttc cgaactctct gccctagagc aagagcaagt cgtctctgtg caccgacagc 120
agacgcaaga gttgatecag gccacgcacg tgagcctgac cctgtggcaa ggcctgttga 180
tcattgaaaa gcaaaaacaa gtcttagaac agcagcaagt gcaagaggcg tactagatag 240
agatcgtaga gatgatectc gccctcgtga ttctggcggc gccctagat ctggacatag 300
agttggaaca acatctggat gatctatgct tcgtcataga aagtacctgc atttgagatg 360
tcctctcttg catctatctg atagaogttg gcgtaacacg acagatctca ctattatccc 420
taggcggacg attgtttcgg gc                                     442
```

*210 - 40

*211 - 135

*212 - FRT

*213 - Artificial Sequence

*220 -

*223 - Description of Artificial Sequence:synthetic
HisNeublastin

<400> 40

Met Gly His His His His His His His His His Ser Ser Gly His
1 5 10 15

Ile Asp Asp Asp Asp Lys Ala Gly Gly Pro Gly Ser Arg Ala Arg Ala
20 25 30

Ala Gly Ala Arg Gly Cys Arg Leu Arg Ser Gln Leu Val Pro Val Arg
35 40 45

Ala Leu Gly Leu Gly His Arg Ser Asp Glu Leu Val Arg Phe Arg Phe
50 55 60

Cys Ser Gly Ser Cys Arg Arg Ala Arg Ser Pro His Asp Leu Ser Leu
65 70 75 80

Ala Ser Leu Leu Gly Ala Gly Ala Leu Arg Pro Pro Pro Gly Ser Arg
85 90 95

Pro Val Ser Gln Pro Cys Cys Arg Pro Thr Arg Tyr Glu Ala Val Ser
100 105 110

Phe Met Asp Val Asn Ser Thr Trp Arg Thr Val Asp Arg Leu Ser Ala
115 120 125

Thr Ala Cys Gly Cys Leu Gly
130 135